



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/509,853

DATE: 10/08/2004
TIME: 13:50:54

Input Set : A:\sequence listing.txt
Output Set: N:\CRF4\10082004\J509853.raw

3 <110> APPLICANT: OriGene Technologies, Inc
5 <120> TITLE OF INVENTION: NOVEL EXPRESSED GENES
7 <130> FILE REFERENCE: 16U 100 PCT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/509,853
C--> 9 <141> CURRENT FILING DATE: 2004-10-01
9 <150> PRIOR APPLICATION NUMBER: US 10/112,372
10 <151> PRIOR FILING DATE: 2002-04-01
12 <150> PRIOR APPLICATION NUMBER: US 60/382,614
13 <151> PRIOR FILING DATE: 2002-05-24
15 <150> PRIOR APPLICATION NUMBER: US 10/164,717
16 <151> PRIOR FILING DATE: 2002-06-10
18 <150> PRIOR APPLICATION NUMBER: US 10/167,631
19 <151> PRIOR FILING DATE: 2002-06-13
21 <150> PRIOR APPLICATION NUMBER: US 10/177,917
22 <151> PRIOR FILING DATE: 2002-06-24
24 <150> PRIOR APPLICATION NUMBER: US 60/399,125
25 <151> PRIOR FILING DATE: 2002-07-30
27 <160> NUMBER OF SEQ ID NOS: 59
29 <170> SOFTWARE: PatentIn version 3.1
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 5536
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (242)..(646)
39 <223> OTHER INFORMATION:

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46 gctaacgaaa gcatgtctga aacaaagcat aactcggtc accggttttc cagtgttgac 180
48 ctgggggtact gaagcagata gtgtccatat atagatctc accctctgca ctctggggcg 240
50 c atg gct gac ttc cag ctt cca gat agt att ctc tgg tgc caa aac cta 289
51 Met Ala Asp Phe Gln Leu Pro Asp Ser Ile Leu Trp Cys Gln Asn Leu
52 1 5 10 15
54 ttt tct ctg cct gtt tgg cag tct gga cat act aga gaa ttg atg ctc 337
55 Phe Ser Leu Pro Val Trp Gln Ser Gly His Thr Arg Glu Leu Met Leu
56 20 25 30
58 cag tgt tca gcc ttg agt gat ggg gaa ctg gtg tat aaa tat ccc agc 385
59 Gln Cys Ser Ala Leu Ser Asp Gly Glu Leu Val Tyr Lys Tyr Pro Ser
60 35 40 45
62 tcc ctc act cct tgg ttg agg tta act ctg ggg tgc atg ttc tac act 433
63 Ser Leu Thr Pro Trp Leu Arg Leu Thr Leu Gly Cys Met Phe Tyr Thr



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66	ggg tcc cag ggt gtc ctc act gag att aag cat cca ctg ccc act gta	481		
67	Gly Ser Gln Gly Val Leu Thr Glu Ile Lys His Pro Leu Pro Thr Val			
68	65	70	75	80
70	ata gct ggt ttg ata atg cat ctt tta ttg tct ccc tct ctc ctc tgc	529		
71	Ile Ala Gly Leu Ile Met His Leu Leu Leu Ser Pro Ser Leu Leu Cys			
72		85	90	95
74	atc att tcc aca ctc cat tac aga ggt tcc ttg ccc tct caa att att	577		
75	Ile Ile Ser Thr Leu His Tyr Arg Gly Ser Leu Pro Ser Gln Ile Ile			
76		100	105	110
78	agc act cat ttt cca tct cga ctt cta aga atc cag att aga cag gca	625		
79	Ser Thr His Phe Pro Ser Arg Leu Leu Arg Ile Gln Ile Arg Gln Ala			
80		115	120	125
82	tta ttt cat ttg gcc att aag tagatcttgt ggaagctgga ttttcatgcc	676		
83	Leu Phe His Leu Ala Ile Lys			
84	130	135		
86	ataccccgaa agtaggcttt tatgtagaca tcatggaggg tgagggctga gatggaagaa	736		
88	gaggtaaaat tggaccaagg aagagaaccc tgggtgtaagg gttccagctc ttaaaagggg	796		
90	gtcctgggta cctggagggc attattacca gatgacagag gatctggagt ggctcttgct	856		
92	aataagtatc ttgggacaaa gagcagttgc atgcacagag agaaactccc aatgcatgaa	916		
94	gaggagctct tcaaagatga attatgagag gcctattata taaataagga ggcaaaaaga	976		
96	agcaaaggag aaccatcctg ttgtatcaat gtcggagggg ggtgactgtt tgcaccttat	1036		
98	gtgccagaga gagtggctga ctaggaaggc aataccagg gatggaaggg cagaggcaag	1096		
100	accatgggag gccccttttt cagcccatca gatgctcaca actctaattgt ctctcttgca	1156		
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104	tcctcttctt gtggagtga tggagagctc tgcagaaggg ggagtctggg gtttaggaga	1276		
106	ccattaaact atctgaatat ctctgatgat gactttgtga aaatgctcct accacctgga	1336		
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120	accataagg agcacctttt tttttcattt aaaaaattta attattatgg ctacataata	1756		
122	gttgtatata ttacagggg atatgtgatg ttccataca ggcatacact atgtaaggat	1816		
124	cagatcaggg taattgtgca tccatctcct caagcatgta tcatttcttt gtgttgga	1876		
126	cattccaaatt acactctttt agttatttta aaatataaga aaaattattg ctaattctcc	1936		
128	cagagtgttg ggattacagg cgtgagccac catgctcggg cttagaagag aataatttga	1996		
130	atgctcccag cataaagaaa ggataaatgt ttaagggtgat ggatatctat ctctattacc	2056		
132	ctgatctgat cattacacat tatgtgaatg tatcgaaata tcacatata tccaaaaata	2116		
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140	accagctgg atcccacctg ggcctgatca cccagttgtc tctacaataa atgaagtcag	2356		
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146	tggccctgcc ctgagcaagc tccaaaccca gtcagagaga tggccaataa aataagcaac	2536		
148	tactgtaccg aggaacaggg ctgtggcaaa caaatgacac tcatttttga atgagtgagt	2596		
150	gaattcaaga ttcagtgaat gaatgaagtg cagtgtattg tgctatctg gtctggagga	2656		

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152 tgagagaagg ctttctagaa gaggtgatag gacacctgga ggatgaataa atttagccat 2716
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156 ggtagaaca agatgggatg gcagaaccaa gaaaactcga atctgaatca gtcagcttag 2836
158 gctgtggggg ccagggtggg atggtgtgga agagatgcta tttgtgaagt aggcaggacc 2896
160 ggggtgtaaa aaacactgtc atccatgtca aagagttag atccattcaa agaaatggga 2956
162 tttttaaaca tgcaggagag gttggtatgt ttaggcacca aatttaacct aatgagaaca 3016
164 tttcaatagt gcctttatcc ctgttttctg gtgatgatgg aaaagcataa tgcctttag 3076
166 atttctcagt tctgaccaca caagttacat gtggataagt cagagccagg tggtgatact 3136
168 ctgaaagtat ccctgtgagc tcagagtgtt ggggttgagaa gatgaacaag gctagatcca 3196
170 cttctatata cactagccca gaggggacct acattcaaga aatccttgcc tacggggatc 3256
172 catggtgcac caggaaaaat gaaattcgta gtcaagacta ggaacaagta cttgggagag 3316
174 aaaggccccc cctggcagcc tccaggtagc aaaccacaag ataatgaaaa ttattgtact 3376
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188 ttattttgag gtcccttctc ccaaagcaaa gctatccagt gtgccaatgca ggtaaagtgg 3796
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208 cacatccaac accatgatgg ggcttacaca catgcatata gacccctcag cctgaacatc 4396
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234 cccgtcaagg gcacttaaaa aacaaaact caaagttcag ggccaagttt gaggatgtgc 5176
236 agaaaggtgt gtgttttttc ttgtcaattg cgactctaat gatggactca cggtgcccgc 5236
238 tcttcccttt ctcttacacc ttacctacct actaaaggag gagttcttgc ttggtaagt 5296
240 gatataatcc gcaaagacat gagagaatgt attagaagcc actcaagagc cttagctacc 5356
242 ttctacaagg ggaaaaggac acacacaaat atctatagt accctttttt tcgtttatgt 5416
244 ttggtcagac tgtttaactt ccattttttt tgtccctccc tttcttttcc ctttagttg 5476
246 aaaactgcta aaatgtcagt ttgcgacct gactttatat ttaaaaaaaaa aaaaaaaaaa 5536
249 <210> SEQ ID NO: 2

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252 <213> ORGANISM: Homo sapiens
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257 1          5          10          15
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261          20          25          30
264 Gln Cys Ser Ala Leu Ser Asp Gly Glu Leu Val Tyr Lys Tyr Pro Ser
265          35          40          45
268 Ser Leu Thr Pro Trp Leu Arg Leu Thr Leu Gly Cys Met Phe Tyr Thr
269          50          55          60
272 Gly Ser Gln Gly Val Leu Thr Glu Ile Lys His Pro Leu Pro Thr Val
273 65          70          75          80
276 Ile Ala Gly Leu Ile Met His Leu Leu Leu Ser Pro Ser Leu Leu Cys
277          85          90          95
280 Ile Ile Ser Thr Leu His Tyr Arg Gly Ser Leu Pro Ser Gln Ile Ile
281          100         105         110
284 Ser Thr His Phe Pro Ser Arg Leu Leu Arg Ile Gln Ile Arg Gln Ala
285          115         120         125
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289          130         135
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293 <211> LENGTH: 26
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302 <211> LENGTH: 25
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306 <400> SEQUENCE: 4
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320 <211> LENGTH: 50
321 <212> TYPE: DNA
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324 <400> SEQUENCE: 6
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328 <210> SEQ ID NO: 7
329 <211> LENGTH: 50
330 <212> TYPE: DNA

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338 <211> LENGTH: 50
339 <212> TYPE: DNA
340 <213> ORGANISM: Homo sapiens
342 <400> SEQUENCE: 8
343 agaaagagtt tataataact ctgatgtctg gatatggttt aatggatccg      50
346 <210> SEQ ID NO: 9
347 <211> LENGTH: 50
348 <212> TYPE: DNA
349 <213> ORGANISM: Homo sapiens
351 <400> SEQUENCE: 9
352 ccaagagggga ttaaaaaggt cgagatggga gagatggagc aatacacttc      50
355 <210> SEQ ID NO: 10
356 <211> LENGTH: 50
357 <212> TYPE: DNA
358 <213> ORGANISM: Homo sapiens
360 <400> SEQUENCE: 10
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364 <210> SEQ ID NO: 11
365 <211> LENGTH: 2270
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367 <213> ORGANISM: Homo sapiens
369 <220> FEATURE:
370 <221> NAME/KEY: CDS
371 <222> LOCATION: (157)..(1080)
372 <223> OTHER INFORMATION:
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379 tgggggactg tgtgagctgg aaacgtggct ggccag atg ggc agc acc atg gag      174
380                                     Met Gly Ser Thr Met Glu
381                                     1               5
383 ccc cct ggg ggt gcg tac ctg cac ctg ggc gcc gtg aca tcc cct gtg      222
384 Pro Pro Gly Gly Ala Tyr Leu His Leu Gly Ala Val Thr Ser Pro Val
385          10               15               20
387 ggc aca gcc cgc gtg ctg cag ctg gcc ttt ggc tgc act acc ttc agc      270
388 Gly Thr Ala Arg Val Leu Gln Leu Ala Phe Gly Cys Thr Thr Phe Ser
389          25               30               35
391 ctg gtg gct cac cgg ggt ggc ttt gcg ggc gtc cag ggc acc ttc tgc      318
392 Leu Val Ala His Arg Gly Gly Phe Ala Gly Val Gln Gly Thr Phe Cys
393          40               45               50
395 atg gcc gcc tgg ggc ttc tgc ttc gcc gtc tct gcg ctg gtg gtg gcc      366
396 Met Ala Ala Trp Gly Phe Cys Phe Ala Val Ser Ala Leu Val Val Ala
397 55          60          65          70
399 tgt gag ttc aca cgg ctc cac ggc tgc ctg cgg ctc tcc tgg ggc aac      414
400 Cys Glu Phe Thr Arg Leu His Gly Cys Leu Arg Leu Ser Trp Gly Asn

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VERIFICATION SUMMARY

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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